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RAW SEQUENCE LISTING

DATE: 06/24/2002

PATENT APPLICATION: US/09/977,260

TIME: 17:54:31

Input Set : A:\38621260.app

Output Set: N:\CRF3\06242002\I977260.raw

p.6

3 <110> APPLICANT: ULLRICH, AXEL
 4 GISHIZKY, MIKHAIL
 5 SURES, IRMINGARD
 7 <120> TITLE OF INVENTION: NOVEL MEGAKARYOCYTIC PROTEIN TYROSINE KINASES
 9 <130> FILE REFERENCE: 038602/1260
 11 <140> CURRENT APPLICATION NUMBER: 09/977,260
 12 <141> CURRENT FILING DATE: 2001-10-16
 14 <150> PRIOR APPLICATION NUMBER: 08/232,545
 15 <151> PRIOR FILING DATE: 1994-04-22
 17 <160> NUMBER OF SEQ ID NOS: 24
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 22 <211> LENGTH: 2000
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 39 aggtcgggtc cagtggcacc cagctcccta cctcctgtgc cagccgctg gcctgtggca 180
 41 ggccattccc agcgtcccg actgtgacca cttgtcagt gtgcctctca cctgcctcag 240
 43 ttccctctg gggggcg atg gcg ggg cga ggc tct ctg gtt tcc tgg cgg 290
 44 Met Ala Gly Arg Gly Ser Leu Val Ser Trp Arg
 45 1 5 10
 47 gca ttt cac ggc tgt gat tct gct gag gaa ctt ccc cgg gtg agc ccc 338
 48 Ala Phe His Gly Cys Asp Ser Ala Glu Glu Leu Pro Arg Val Ser Pro
 49 15 20 25
 51 cgc ttc ctc cga gcc tgg cac ccc cct ccc gtc tca gcc agg atg cca 386
 52 Arg Phe Leu Arg Ala Trp His Pro Pro Pro Val Ser Ala Arg Met Pro
 53 30 35 40
 55 acg agg cgc tgg gcc ccg ggc acc cag tgt atc acc aaa tgc gag cac 434
 56 Thr Arg Arg Trp Ala Pro Gly Thr Gln Cys Ile Thr Lys Cys Glu His
 57 45 50 55
 59 acc cgc ccc aag cca ggg gag ctg gcc ttc cgc aag ggc gac gtg gtc 482
 60 Thr Arg Pro Lys Pro Gly Glu Leu Ala Phe Arg Lys Gly Asp Val Val
 61 60 65 70 75
 63 acc atc ctg gag gcc tgc gag aac aag agc tgg tac cgc gtc aag cac 530
 64 Thr Ile Leu Glu Ala Cys Glu Asn Lys Ser Trp Tyr Arg Val Lys His

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65	80	85	90	
67	cac acc agt gga cag gag ggg ctg ctg gca gct ggg gcg ctg cgg gag	578		
68	His Thr Ser Gly Gln Glu Gly Leu Leu Ala Ala Gly Ala Leu Arg Glu			
69	95 100 105			
71	cgg gag gcc ctc tcc gca gac ccc aag ctc agc ctc atg ccg tgg ttc	626		
72	Arg Glu Ala Leu Ser Ala Asp Pro Lys Leu Ser Leu Met Pro Trp Phe			
73	110 115 120			
75	cac ggg aag atc tcg ggc cag gag gct gtc cag cag ctg cag cct ccc	674		
76	His Gly Lys Ile Ser Gly Gln Glu Ala Val Gln Gln Leu Gln Pro Pro			
77	125 130 135			
79	gag gat ggg ctg ttc ctg gtg cgg gag tcc gcg cgc cac ccc ggc gac	722		
80	Glu Asp Gly Leu Phe Leu Val Arg Glu Ser Ala Arg His Pro Gly Asp			
81	140 145 150 155			
83	tac gtc ctg tgc gtg agc ttt ggc cgc gac gtc atc cac tac cgc gtg	770		
84	Tyr Val Leu Cys Val Ser Phe Gly Arg Asp Val Ile His Tyr Arg Val			
85	160 165 170			
87	ctg cac cgc gac ggc cac ctc aca atc gat gag gcc gtg ttc ttc tgc	818		
88	Leu His Arg Asp Gly His Leu Thr Ile Asp Glu Ala Val Phe Phe Cys			
89	175 180 185			
91	aac ctc atg gac atg gtg gag cat tac agc aag gac aag ggc gct atc	866		
92	Asn Leu Met Asp Met Val Glu His Tyr Ser Lys Asp Lys Gly Ala Ile			
93	190 195 200			
95	tgc acc aag ctg gtg aga cca aag cgg aaa cac ggg acc aag tcg gcc	914		
96	Cys Thr Lys Leu Val Arg Pro Lys Arg Lys His Gly Thr Lys Ser Ala			
97	205 210 215			
99	gag gag gag ctg gcc agg gcg ggc tgg tta ctg aac ctg cag cat ttg	962		
100	Glu Glu Glu Leu Ala Arg Ala Gly Trp Leu Leu Asn Leu Gln His Leu			
101	220 225 230 235			
103	aca ttg gga gca cag atc gga gag gga gag ttt gga gct gtc ctg cag	1010		
104	Thr Leu Gly Ala Gln Ile Gly Glu Gly Glu Phe Gly Ala Val Leu Gln			
105	240 245 250			
107	ggt gag tac ctg ggg caa aag gtg gcc gtg aag aat atc aag tgt gat	1058		
108	Gly Glu Tyr Leu Gly Gln Lys Val Ala Val Lys Asn Ile Lys Cys Asp			
109	255 260 265			
111	gtg aca gcc cag gcc ttc ctg gac gag acg gcc gtc atg acg aag atg	1106		
112	Val Thr Ala Gln Ala Phe Leu Asp Glu Thr Ala Val Met Thr Lys Met			
113	270 275 280			
115	caa cac gag aac ctg gtg cgt ctc ctg ggc gtg atc ctg cac cag ggg	1154		
116	Gln His Glu Asn Leu Val Arg Leu Leu Gly Val Ile Leu His Gln Gly			
117	285 290 295			
119	ctg tac att gtc atg gag cac gtg agc aag ggc aac ctg gtg aac ttt	1202		
120	Leu Tyr Ile Val Met Glu His Val Ser Lys Gly Asn Leu Val Asn Phe			
121	300 305 310 315			
123	ctg cgg acc cgg ggt cga gcc ctc gtg aac acc gct cag ctc ctg cag	1250		
124	Leu Arg Thr Arg Gly Arg Ala Leu Val Asn Thr Ala Gln Leu Leu Gln			
125	320 325 330			
127	ttt tct ctg cac gtg gcc gag ggc atg gag tac ctg gag agc aag aag	1298		
128	Phe Ser Leu His Val Ala Glu Gly Met Glu Tyr Leu Glu Ser Lys Lys			
129	335 340 345			

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131 ctt gtg cac cgc gac ctg gcc gcc cgc aac atc ctg gtc tca gag gac 1346
132 Leu Val His Arg Asp Leu Ala Ala Arg Asn Ile Leu Val Ser Glu Asp
133      350      355      360
135 ctg gtg gcc aag gtc agc gac ttt ggc ctg gcc aaa gcc gag cgg aag 1394
136 Leu Val Ala Lys Val Ser Asp Phe Gly Leu Ala Lys Ala Glu Arg Lys
137      365      370      375
139 ggg cta gac tca agc cgg ctg ccc gtc aag tgg acg gcg ccc gag gct 1442
140 Gly Leu Asp Ser Ser Arg Leu Pro Val Lys Trp Thr Ala Pro Glu Ala
141 380      385      390      395
143 ctc aaa cac ggg aag ttc acc agc aag tcg gat gtc tgg agt ttt ggg 1490
144 Leu Lys His Gly Lys Phe Thr Ser Lys Ser Asp Val Trp Ser Phe Gly
145      400      405      410
147 gtg ctg ctc tgg gag gtc ttc tca tat gga cgg gct ccg tac cct aaa 1538
148 Val Leu Leu Trp Glu Val Phe Ser Tyr Gly Arg Ala Pro Tyr Pro Lys
149      415      420      425
151 atg tca ctg aaa gag gtg tcg gag gcc gtg gag aag ggg tac cgc atg 1586
152 Met Ser Leu Lys Glu Val Ser Glu Ala Val Glu Lys Gly Tyr Arg Met
153      430      435      440
155 gaa ccc ccc gag ggc tgt cca ggc ccc gtg cac gtc ctc atg agc agc 1634
156 Glu Pro Pro Glu Gly Cys Pro Gly Pro Val His Val Leu Met Ser Ser
157      445      450      455
159 tgc tgg gag gca gag ccc gcc cgc cgg cca ccc ttc cgc aaa ctg gcc 1682
160 Cys Trp Glu Ala Glu Pro Ala Arg Arg Pro Pro Phe Arg Lys Leu Ala
161 460      465      470      475
163 gag aag ctg gcc cgg gag cta cgc agt gca ggt gcc cca gcc tcc gtc 1730
164 Glu Lys Leu Ala Arg Glu Leu Arg Ser Ala Gly Ala Pro Ala Ser Val
165      480      485      490
167 tca ggg cag gac gcc gac ggc tcc acc tcg ccc cga agc cag gag ccc -1778
168 Ser Gly Gln Asp Ala Asp Gly Ser Thr Ser Pro Arg Ser Gln Glu Pro
169      495      500      505
171 tgacccacc cgggtgggcc cttggcccca gaggaccgag agagtggaga gtgcggcgtg 1838
173 ggggcactga ccaggcccaa ggagggtcca ggcgggcaag tcatacctcct ggtgccca 1898
175 gcaggggctg gccacgtag ggggctctgg gcggcccgtg gacacccag acctgcgaag 1958
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186 <223> OTHER INFORMATION: Description of Unknown Organism: Megakaryocyte
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189 <400> SEQUENCE: 2
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196 Trp His Pro Pro Pro Val Ser Ala Arg Met Pro Thr Arg Arg Trp Ala
197      35      40      45
199 Pro Gly Thr Gln Cys Ile Thr Lys Cys Glu His Thr Arg Pro Lys Pro

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203 65      70      75      80
205 Cys Glu Asn Lys Ser Trp Tyr Arg Val Lys His His Thr Ser Gly Gln
206      85      90      95
208 Glu Gly Leu Leu Ala Ala Gly Ala Leu Arg Glu Arg Glu Ala Leu Ser
209      100      105      110
211 Ala Asp Pro Lys Leu Ser Leu Met Pro Trp Phe His Gly Lys Ile Ser
212      115      120      125
214 Gly Gln Glu Ala Val Gln Gln Leu Gln Pro Pro Glu Asp Gly Leu Phe
215      130      135      140
217 Leu Val Arg Glu Ser Ala Arg His Pro Gly Asp Tyr Val Leu Cys Val
218 145      150      155      160
220 Ser Phe Gly Arg Asp Val Ile His Tyr Arg Val Leu His Arg Asp Gly
221      165      170      175
223 His Leu Thr Ile Asp Glu Ala Val Phe Phe Cys Asn Leu Met Asp Met
224      180      185      190
226 Val Glu His Tyr Ser Lys Asp Lys Gly Ala Ile Cys Thr Lys Leu Val
227      195      200      205
229 Arg Pro Lys Arg Lys His Gly Thr Lys Ser Ala Glu Glu Glu Leu Ala
230      210      215      220
232 Arg Ala Gly Trp Leu Leu Asn Leu Gln His Leu Thr Leu Gly Ala Gln
233 225      230      235      240
235 Ile Gly Glu Gly Glu Phe Gly Ala Val Leu Gln Gly Glu Tyr Leu Gly
236      245      250      255
238 Gln Lys Val Ala Val Lys Asn Ile Lys Cys Asp Val Thr Ala Gln Ala
239      260      265      270
241 Phe Leu Asp Glu Thr Ala Val Met Thr Lys Met Gln His Glu Asn Leu
242      275      280      285
244 Val Arg Leu Leu Gly Val Ile Leu His Gln Gly Leu Tyr Ile Val Met
245      290      295      300
247 Glu His Val Ser Lys Gly Asn Leu Val Asn Phe Leu Arg Thr Arg Gly
248 305      310      315      320
250 Arg Ala Leu Val Asn Thr Ala Gln Leu Leu Gln Phe Ser Leu His Val
251      325      330      335
253 Ala Glu Gly Met Glu Tyr Leu Glu Ser Lys Lys Leu Val His Arg Asp
254      340      345      350
256 Leu Ala Ala Arg Asn Ile Leu Val Ser Glu Asp Leu Val Ala Lys Val
257      355      360      365
259 Ser Asp Phe Gly Leu Ala Lys Ala Glu Arg Lys Gly Leu Asp Ser Ser
260      370      375      380
262 Arg Leu Pro Val Lys Trp Thr Ala Pro Glu Ala Leu Lys His Gly Lys
263 385      390      395      400
265 Phe Thr Ser Lys Ser Asp Val Trp Ser Phe Gly Val Leu Leu Trp Glu
266      405      410      415
268 Val Phe Ser Tyr Gly Arg Ala Pro Tyr Pro Lys Met Ser Leu Lys Glu
269      420      425      430
271 Val Ser Glu Ala Val Glu Lys Gly Tyr Arg Met Glu Pro Pro Glu Gly
272      435      440      445

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Output Set: N:\CRF3\06242002\I977260.raw

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274 Cys Pro Gly Pro Val His Val Leu Met Ser Ser Cys Trp Glu Ala Glu
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277 Pro Ala Arg Arg Pro Pro Phe Arg Lys Leu Ala Glu Lys Leu Ala Arg
278 465      470      475      480
280 Glu Leu Arg Ser Ala Gly Ala Pro Ala Ser Val Ser Gly Gln Asp Ala
281      485      490      495
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288 <211> LENGTH: 2500
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293 <221> NAME/KEY: CDS
294 <222> LOCATION: (82)..(2106)
296 <220> FEATURE:
297 <223> OTHER INFORMATION: Description of Unknown Organism: Megakaryocyte
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303 agcgagtcta aggatgataa t atg gat aca aaa tct att cta gaa gaa ctt 111
304      Met Asp Thr Lys Ser Ile Leu Glu Glu Leu
305      1      5      10
307 ctt ctc aaa aga tca cag caa aag aag aaa atg tca cca aat aat tac 159
308 Leu Leu Lys Arg Ser Gln Gln Lys Lys Lys Met Ser Pro Asn Asn Tyr
309      15      20      25
311 aaa gaa cgg ctt ttt gtt ttg acc aaa aca aac ctt tcc tac tat gaa 207
312 Lys Glu Arg Leu Phe Val Leu Thr Lys Thr Asn Leu Ser Tyr Tyr Glu
313      30      35      40
315 tat gac aaa atg aaa agg ggc agc aga aaa gga tcc att gaa att aag 255
316 Tyr Asp Lys Met Lys Arg Gly Ser Arg Lys Gly Ser Ile Glu Ile Lys
317      45      50      55
319 aaa atc aga tgt gtg gag aaa gta aat ctc gag gag cag acg cct gta 303
320 Lys Ile Arg Cys Val Glu Lys Val Asn Leu Glu Glu Gln Thr Pro Val
321      60      65      70
323 gag aga cag tac cca ttt cag att gtc tat aaa gat ggg ctt ctc tat 351
324 Glu Arg Gln Tyr Pro Phe Gln Ile Val Tyr Lys Asp Gly Leu Leu Tyr
325 75      80      85      90
327 gtc tat gca tca aat gaa gag agc cga agt cag tgg ttg aaa gca tta 399
328 Val Tyr Ala Ser Asn Glu Glu Ser Arg Ser Gln Trp Leu Lys Ala Leu
329      95      100      105
331 caa aaa gag ata agg ggt aac ccc cac ctg ctg gtc aag tac cat agt 447
332 Gln Lys Glu Ile Arg Gly Asn Pro His Leu Leu Val Lys Tyr His Ser
333      110      115      120
335 ggg ttc ttc gtg gac ggg aag ttc ctg tgt tgc cag cag agc tgt aaa 495
336 Gly Phe Phe Val Asp Gly Lys Phe Leu Cys Cys Gln Gln Ser Cys Lys
337      125      130      135
339 gca gcc cca gga tgt acc ctc tgg gaa gca tat gct aat ctg cat act 543
340 Ala Ala Pro Gly Cys Thr Leu Trp Glu Ala Tyr Ala Asn Leu His Thr

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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/09/977,260

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:20; N Pos. 14,20,23,26

Seq#:21; N Pos. 12,18,24

Seq#:24; Xaa Pos. 6